APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/813,507	03/30/2004	John S. Lollar	13097/3	5299

757   7590   07/31/2007
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P.O. BOX 10395
CHICAGO, IL 60610

EXAMINER
GIBBS, TERRA C

ART UNIT	PAPER NUMBER
1635	

MAIL DATE	DELIVERY MODE
07/31/2007	PAPER

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The time period for reply, if any, is set in the attached communication.

UNITED STATES DEPARTMENT OF COMMERCE
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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
10813507	3/30/04	LOLLAR, JOHN S.	13097/3

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EXAMINER
Terra C. Gibbs

ART UNIT	PAPER
1635	7252007

DATE MAILED:

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Commissioner for Patents

Notice to Comply with the Sequence Rules

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. §1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §1.821-1.825 for the reason(s) set forth on the attached Sequence Listing Error Report. Applicant must fully comply with the sequence rules for any response to this action to be considered fully responsive.

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES of 37 C.F.R. §1.821-1.825. Failure to comply with these requirements will result in ABANDOMENT of the application under 37 C.F.R. §1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. §1.136. In no case may an applicant extend the period for response beyond the six-month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Terra C. Gibbs whose telephone number is 571-272-0758. The examiner can normally be reached on 9 am - 5 pm M-F.
If attempts to reach the examiner by telephone are unsuccessful, the Examiner's supervisor, James Schultz can be reached on 571-272-0763. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.
Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

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tcg
July 25, 2007

/Terra C. Gibbs/

==

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Mon Jun 11 13:25:27 EDT 2007

==

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Reviewer Comments:

seq Id 6:

Missing amino acid numbering, they non-aligned 645,650,655

Please delete text appearing after seq id 21.

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Application No: 10813507   Version No: 2.0

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Total Errors:	681
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Actual SeqID Count:	21

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W 112	Upper case found in data; Found at position(3) SeqId(6)
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E 342	'n' position not defined found at POS: 15 SEQID(6)
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W 112	Upper case found in data; Found at position(45) SeqId(6)
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E 323	Invalid/missing amino acid numbering SEQID (6) POS (649)

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              Output Set:



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E 323	Invalid/missing amino acid numbering SEQID (6) POS (689)
E 323	Invalid/missing amino acid numbering SEQID (6)at Protein (690) This error has occured more than 20 times, will not be displayed
E 331	Count of Protein differs from the <211> tag Input: 2351 Calculated: 2335 SEQID(6)
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<110> Lollar, John S.

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<141> 2004-03-30

<150> PCT/US02/33403
<151> 2002-10-07

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Gly Phe Ser Ala Ile Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
                20                  25                  30

tgg gac tac cgg caa agt gaa ctc ctc cgt gag ctg cac gtg gac acc   144
Trp Asp Tyr Arg Gln Ser Glu Leu Leu Arg Glu Leu His Val Asp Thr
            35                  40                  45

aga ttt cct gct aca gcg cca gga gct ctt ccg ttg ggc ccg tca gtc   192
Arg Phe Pro Ala Thr Ala Pro Gly Ala Leu Pro Leu Gly Pro Ser Val
        50                  55                  60

ctg tac aaa aag act gtg ttc gta gag ttc acg gat caa ctt ttc agc   240
Leu Tyr Lys Lys Thr Val Phe Val Glu Phe Thr Asp Gln Leu Phe Ser
 65                  70                  75                  80
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Val Ala Arg Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
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cag gct gag gtt tac gac acg gtg gtc gtt acc ctg aag aac atg gct    336
Gln Ala Glu Val Tyr Asp Thr Val Val Val Thr Leu Lys Asn Met Ala
            100                 105                 110

tct cat ccc gtt agt ctt cac gct gtc ggc gtc tcc ttc tgg aaa tct    384
Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Phe Trp Lys Ser
        115                 120                 125

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Ser Glu Gly Ala Glu Tyr Glu Asp His Thr Ser Gln Arg Glu Lys Glu
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gac gat aaa gtc ctt ccc ggt aaa agc caa acc tac gtc tgg cag gtc    480
Asp Asp Lys Val Leu Pro Gly Lys Ser Gln Thr Tyr Val Trp Gln Val
145                 150                 155                 160

ctg aaa gaa aat ggt cca aca gcc tct gac cca cca tgt ctc acc tac    528
Leu Lys Glu Asn Gly Pro Thr Ala Ser Asp Pro Pro Cys Leu Thr Tyr
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tca tac ctg tct cac gtg gac ctg gtg aaa gac ctg aat tcg ggc ctc    576
Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu
            180                 185                 190

att gga gcc ctg ctg gtt tgt aga gaa ggg agt ctg acc aga gaa agg    624
Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Thr Arg Glu Arg
        195                 200                 205

acc cag aac ctg cac gaa ttt gta cta ctt ttt gct gtc ttt gat gaa    672
Thr Gln Asn Leu His Glu Phe Val Leu Leu Phe Ala Val Phe Asp Glu
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Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Lys Lys Ser
            260                 265                 270

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Val Tyr Trp His Val Ile Gly Met Gly Thr Ser Pro Glu Val His Ser
        275                 280                 285

att ttt ctt gaa ggc cac acg ttt ctc gtg agg cac cat cgc cag gct    912
Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg His His Arg Gln Ala
    290                 295                 300
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atg gac ctt ggc cag ttc cta ctg ttt tgt cat atc tct tcc cac cac     1008
Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His His
                325                 330                 335

cat ggt ggc atg gag gct cac gtc aga gta gaa agc.tgc gcc gag gag     1056
His Gly Gly Met Glu Ala His Val Arg Val Glu Ser Cys Ala Glu Glu
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ccc cag ctg cgg agg aaa gct gat gaa gag gaa gat tat gat gac aat     1104
Pro Gln Leu Arg Arg Lys Ala Asp Glu Glu Glu Asp Tyr Asp Asp Asn
        355                 360                 365

ttg tac gac tcg gac atg gac gtg gtc cgg ctc gat ggt gac gac gtg     1152
Leu Tyr Asp Ser Asp Met Asp Val Val Arg Leu Asp Gly Asp Asp Val
    370                 375                 380

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Trp Val His Tyr Ile Ser Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

gcg gtc ccc agc ccc agt gac aga agt tat aaa agt ctc tac ttg aac     1296
Ala Val Pro Ser Pro Ser Asp Arg Ser Tyr Lys Ser Leu Tyr Leu Asn
            420                 425                 430

agt ggt cct cag cga att ggt agg aaa tac aaa aaa gct cga ttc gtc     1344
Ser Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Ala Arg Phe Val
        435                 440                 445

gct tac acg gat gta aca ttt aag act cgt aaa gct att ccg tat gaa     1392
Ala Tyr Thr Asp Val Thr Phe Lys Thr Arg Lys Ala Ile Pro Tyr Glu
        450                 455                 460

tca gga atc ctg gga cct tta ctt tat gga gaa gtt gga gac aca ctt     1440
Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

ttg att ata ttt aag aat aaa gcg agc cga cca tat aac atc tac cct     1488
Leu Ile Ile Phe Lys Asn Lys Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

cat gga atc act gat gtc agc gct ttg cac cca ggg aga ctt cta aaa     1536
His Gly Ile Thr Asp Val Ser Ala Leu His Pro Gly Arg Leu Leu Lys
            500                 505                 510

ggt tgg aaa cat ttg aaa gac atg cca att ctg cca gga gag act ttc     1584
Gly Trp Lys His Leu Lys Asp Met Pro Ile Leu Pro Gly Glu Thr Phe
        515                 520                 525

aag tat aaa tgg aca gtg act gtg.gaa gat ggg cca acc aag tcc gat     1632
Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
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545                 550                 555                 560


gat ctg gct tcg gga ctc att ggc cct ctc ctc atc tgc tac aaa gaa       1728
Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575


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Ser Val Asp Gln Arg Gly Asn Gln Met Met Ser Asp Lys Arg Asn Val
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cca gag ttc caa gct tct aac atc atg cac agc atc aat ggc tat gtt       1920
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625                 630                 635                 640


ttt gat agc ttg cag ctg tcg gtt tgt ttg cac gag gtg gca tac tgg       1968
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tac att cta agt gtt gga gca cag acg gac ttc ctc tcc gtc ttc ttc       2016
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                660                 665                 670


tct ggc tac acc ttc aaa cac aaa atg gtc tat gaa gac aca ctc acc       2064
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
                675                 680                 685


ctg ttc ccc ttc tca gga gaa acg gtc ttc atg tca atg gaa aac cca       2112
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ggt ctc tgg gtc cta ggg tgc cac aac tca gac ttg cgg aac aga ggg       2160
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705                 710                 715                 720


atg aca gcc tta ctg aag gtg tat agt tgt gac agg gac att ggt gat       2208
Met Thr Ala Leu Leu Lys Val Tyr Ser Cys Asp Arg Asp Ile Gly Asp
                725                 730                 735


tat tat gac aac act tat gaa gat att cca ggc ttc ttg ctg agt gga       2256
Tyr Tyr Asp Asn Thr Tyr Glu Asp Ile Pro Gly Phe Leu Leu Ser Gly
                740                 745                 750


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Lys Asn Val Ile Glu Pro Arg Ser Phe Ala Gln Asn Ser Arg Pro Pro
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785   790   795   800

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Thr Leu Ser Ala Glu Thr Glu Arg Thr His Ser Leu Gly Pro Pro His
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ccg cag gtt aat ttc agg agt caa tta ggt gcc att gta ctt ggc aaa   2784
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aat tca tct cac ttt att ggg gct ggt gtc cct ttg ggc tcg act gag   2832
Asn Ser Ser His Phe Ile Gly Ala Gly Val Pro Leu Gly Ser Thr Glu
        930   935   940

gag gat cat gaa agc tcc ctg gga gaa aat gta tca cca gtg gag agt   2880
Glu Asp His Glu Ser Ser Leu Gly Glu Asn Val Ser Pro Val Glu Ser
945   950   955   960

gac ggg ata ttt gaa aag gaa aga gct cat gga cct gct tca ctg acc   2928
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                965   970   975

aaa gac gat gtt tta ttt aaa gtt aat atc tct ttg gta aag aca aac   2976
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    1010                1015                1020


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1025                1030                1035                1040


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                1125                1130                1135


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        1170                1175                1180


gag aga gca gag act cac ata gcc cat ttc tca gca att agg gaa gag    3600
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1185                1190                1195                1200


gca ccc ttg gaa gcc ccg gga aat cga aca ggt cca ggt ccg agg agt    3648
Ala Pro Leu Glu Ala Pro Gly Asn Arg Thr Gly Pro Gly Pro Arg Ser
                1205                1210                1215
```

```
gcg gtt ccc cgc cgc gtt aag cag agc ttg aaa cag atc aga ctc ccg     3696
Ala Val Pro Arg Arg Val Lys Gln Ser Leu Lys Gln Ile Arg Leu Pro
            1220             1225             1230


cta gaa gaa ata aag cct gaa agg ggg gtg gtt ctg aat gcc acc tca     3744
Leu Glu Glu Ile Lys Pro Glu Arg Gly Val Val Leu Asn Ala Thr Ser
            1235             1240             1245


acc cgg tgg tct gaa agc agt cct atc tta caa gga gcc aaa aga aat     3792
Thr Arg Trp Ser Glu Ser Ser Pro Ile Leu Gln Gly Ala Lys Arg Asn
            1250             1255             1260


aac ctt tct tta cct ttc ctg acc ttg gaa atg gcc gga ggt caa gga     3840
Asn Leu Ser Leu Pro Phe Leu Thr Leu Glu Met Ala Gly Gly Gln Gly
1265             1270             1275             1280


aag atc agc gcc ctg ggg aaa agt gcc gca ggc ccg ctg gcg tcc ggg     3888
Lys Ile Ser Ala Leu Gly Lys Ser Ala Ala Gly Pro Leu Ala Ser Gly
            1285             1290             1295


aag ctg gag aag gct gtt ctc tct tca gca ggc ttg tct gaa gca tct     3936
Lys Leu Glu Lys Ala Val Leu Ser Ser Ala Gly Leu Ser Glu Ala Ser
            1300             1305             1310


ggc aaa gct gag ttt ctt cct aaa gtt cga gtt cat cgg gaa gac ctg     3984
Gly Lys Ala Glu Phe Leu Pro Lys Val Arg Val His Arg Glu Asp Leu
            1315             1320             1325


ttg cct caa aaa acc agc aat gtt tct tgc gca cac ggg gat ctc ggc     4032
Leu Pro Gln Lys Thr Ser Asn Val Ser Cys Ala His Gly Asp Leu Gly
            1330             1335             1340


cag gag atc ttc ctg cag aaa aca cgg gga cct gtt aac ctg aac aaa     4080
Gln Glu Ile Phe Leu Gln Lys Thr Arg Gly Pro Val Asn Leu Asn Lys
1345             1350             1355             1360


gta aat aga cct gga agg act ccc tcc aag ctt ctg ggt ccc ccg atg     4128
Val Asn Arg Pro Gly Arg Thr Pro Ser Lys Leu Leu Gly Pro Pro Met
             1365             1370             1375


ccc aaa gag tgg gaa tcc cta gag aag tca cca aaa agc aca gct ctc     4176
Pro Lys Glu Trp Glu Ser Leu Glu Lys Ser Pro Lys Ser Thr Ala Leu
            1380             1385             1390


agg acg aaa gac atc atc agt tta ccc ctg gac cgt cac gaa agc aat     4224
```

	Application No.	Applicant(s)
Notice to Comply	10813507	LOLLAR, JOHN S.
	Examiner	**Art Unit**
	Terra C. Gibbs	1635

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set in the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: Please see attached Sequence Listing Error Form at "Reviewer Comments".

Applicant Must Provide:
☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the specification**.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

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